

BLAST Basic Local Alignment Search ToolSEQ 2

Job Title: BD205212:Nucleotide sequence for detecting...

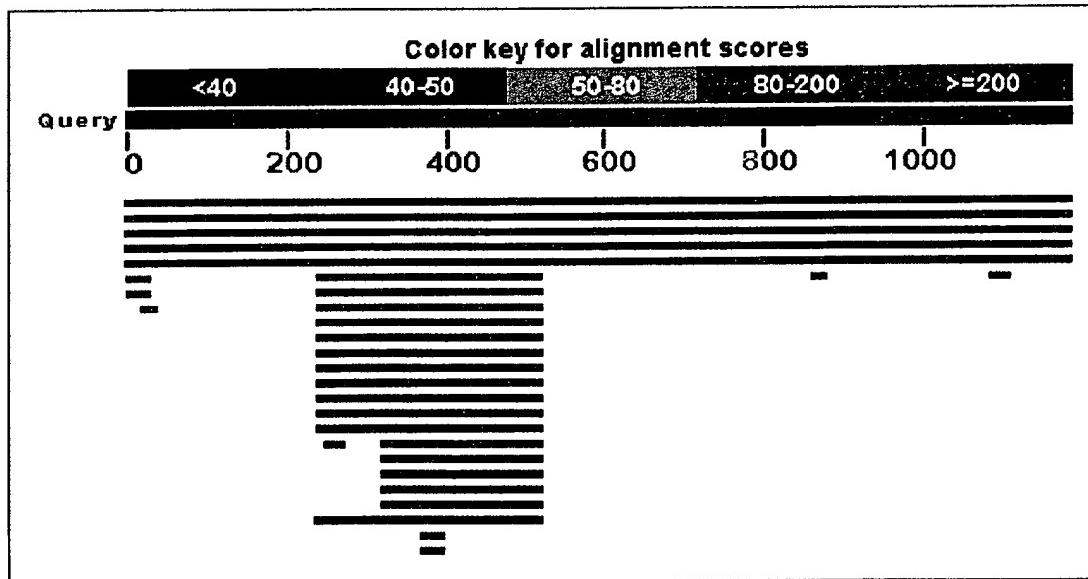
Document 2

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BLASTN 2.2.18+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402. RID: 88NSGD54014 Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences) 7,064,549 sequences; 24,305,219,031 total letters

Query= gi|33014982|dbj|BD205212.1| Nucleotide sequence for detecting enterohemorrhagic Escherichia coli (EHEC) Length=1181

Distribution of 30 Blast Hits on the Query Sequence

Distance tree of results [NEW](#)

Legend for links to other resources: UniGene GEO Gene Structure

Sequences producing significant alignments:

(Click headers to sort columns)

AF401292.1	Escherichia coli O157:H- plasmid pSF0157, complete sequence	2111	2111	100%	0.0	99%
AF074613.1	Escherichia coli O157:H7 plasmid pO157, 2111 2111 complete sequence	2111	2111	100%	0.0	99%
Y11275.1	E.coli 7.4 kb DNA from plasmid pO157	2111	2111	100%	0.0	99%
AB011549.2	Escherichia coli O157:H7 str. Sakai plasmid pO157 DNA, complete sequence	2111	2111	100%	0.0	99%
AF043470.1	Escherichia coli plasmid pO157 ecf4 gene, partial cds; and ecf3, ecf2, and ecf1 genes, complete cds	2102	2102	100%	0.0	99%
CP000035.1	Shigella dysenteriae Sd197 plasmid pSD1_197, complete sequence	138	138	24%	6e-29	71%
CP001064.1	Escherichia coli 53638 plasmid p53638_226, complete sequence	132	132	24%	3e-27	71%
CP001062.1	Shigella boydii CDC 3083-94 plasmid pBS512_211, complete sequence	132	132	24%	3e-27	71%
AF386526.1	Shigella flexneri 2a str. 301 virulence plasmid pCP301, complete sequence	132	132	24%	3e-27	71%
AY206446.1	Shigella flexneri plasmid pINV_F6_M1382 ORF186 (ORF186), VirK (virK), and MsbB2 (msbB2) genes, complete cds	132	132	24%	3e-27	71%
AL391753.1	Shigella flexneri virulence plasmid pWR100: from 1 to 213494	132	132	24%	3e-27	71%
AF348706.1	Shigella flexneri 5a plasmid virulence plasmid pWR501, complete sequence	132	132	24%	3e-27	71%
AY879342.1	Shigella flexneri plasmid pSF5, complete sequence	132	132	24%	3e-27	71%
CP000037.1	Shigella boydii Sb227 plasmid pSB4_227, complete sequence	132	132	24%	3e-27	71%
CP000039.1	Shigella sonnei Ss046 plasmid pSS_046, complete sequence	132	132	24%	3e-27	71%
D11025.1	Shigella flexneri plasmid pMYSH6000 virK gene for virulence protein, complete cds	132	132	24%	3e-27	71%
CP000799.1	Escherichia coli E24377A plasmid pETEC_74, complete sequence	111	111	17%	9e-21	71%
CP000795.1	Escherichia coli E24377A plasmid pETEC_80, complete sequence	111	111	17%	9e-21	71%
AB255435.1	Escherichia coli plasmid pO86A1 DNA, complete sequence	111	111	17%	9e-21	71%
AF134403.1	Escherichia coli plasmid pAA2 Shf (shf), hexosyltransferase homolog (capU), and VirK (virK) genes, complete cds	111	111	17%	9e-21	71%
CR942285.1	Escherichia coli plasmid pCoo	111	111	17%	9e-21	71%
CP000800.1	Escherichia coli E24377A, complete genome	107	107	24%	1e-19	69%
AC133908.7	Mus musculus chromosome 5, clone RP24-299L9, complete sequence	46.4	46.4	2%	0.30	93%
AC127327.4	Mus musculus BAC clone RP23-254M18 from 46.4	46.4	46.4	2%	0.30	93%

5, complete sequence							
EU025714.1	Salmo salar retinoic acid receptor gamma a (Rarga), coiled-coil transcriptional coactivator a (Kiaa1536), homeobox protein HoxC13aa (HoxC13aa), homeobox protein HoxC12aa (HoxC12aa), homeobox protein HoxC11aa (HoxC11aa), homeobox protein HoxC10aa (HoxC10aa), homeobox protein HoxC9aa (HoxC9aa), homeobox protein HoxC8aa (HoxC8aa), and homeobox protein HoxC6aa (HoxC6aa) genes, complete cds		44.6	44.6	2%	1.1	93%
BX571861.1	Photorhabdus luminescens subsp. laumondii TTO1 complete genome; segment 3/17		44.6	44.6	2%	1.1	100%
DQ192243.1	Operophtera brumata reovirus segment 9, complete sequence		42.8	42.8	2%	3.7	92% G
AC145866.3	Pan troglodytes BAC clone RP43-21B7 from chromosome 7, complete sequence		42.8	42.8	2%	3.7	90%
AE015928.1	Bacteroides thetaiotaomicron VPI-5482, complete genome		42.8	42.8	1%	3.7	100%
AC004844.1	Homo sapiens PAC clone RP4-613I23 from 7p11-p13, complete sequence		42.8	42.8	2%	3.7	90% E

Alignments

>gb|AF401292.1| D Escherichia coli O157:H- plasmid pSFO157, complete sequence
Length=121239

Score = 2111 bits (2340), Expect = 0.0
Identities = 1178/1182 (99%), Gaps = 1/1182 (0%)
Strand=Plus/Minus

Query 1	CTGCAGGAGA-TGG	TTGCCCATCCCAGCGCGCTCCAGCT	59
Sbjct 29247			
Query 60	GAAAGTAGGCCTGTTCTGTCCGGTATTTAAATGCATTGACCGTCCCCGTATTTAAACAAT		11
Sbjct 29187			
Query 120	GTGATAAAATTACTCCGTTACCGGAAAACCGCTGAACAAAATTCCGGCTGAAAAGAGGATC		17
Sbjct 29127			
Query 180	CGCCGTATCTGTCATTTCCCTTAGCCTGACTAGCCAGAGACACAATGATCTGTGCC		23
Sbjct 29067			
Query 240	GTTCTGTTAATATCAAACCGGTACTCAATATCTTCTGGCGCTGGCTGCCATCATCCGG		29
Sbjct 29007			
Query 300	AAGCGTTCCGGTCGGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACATCCCC		35
Sbjct 28947			
Query 360	ACGGGTAACAGCGTCCCTGTCACATTCTCTGAATGACATCAGGGATCCGCCGTCTCA		41
Sbjct 28887			
Query 420	CTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAACGCTTCA		47
Sbjct 28827			
Query 480	TTTCCGAAGGCATGACCACACACTGGCAATCCGTAGACCGTAACGCTGGAAAAGG		53
Sbjct 28767			
Query 540	GCACCTGCCATTAACACATCTCGCTCATTCCAGGTGTTCTGCTGACGCAGACGT		59
Sbjct 28707			
Query 600	GCTTCGTATTCTCACGCCGGCCACCACAGGCCAGCGAAATGATTTCCCTTCATC		65
Sbjct 28647			
Query 660	TTCAGCTGATAACAATACACGCAAGCATAAATTCAATGTCCTTTCCGGGACGTAGCATCCC		71
Sbjct 28587			
Query 720	ACCTGAACGATAAGCGGAACATTGTCGATGCAGCCCAGGGTGGATATGCAGGGGT		77
Sbjct 28527			
Query 780	ACCGGTCGATGGCTCATTATGCAATGCCGGCAGTCGAAACCCGGTGGAAATAACCGTT		83
Sbjct 28467			
Query 840	ACCGGTTGCTGACACCTCCGCCATCAGATGCGCCATCATGGGTGAGATAGGCACAACA		89
Sbjct 28407			
Query 900	ATGAAATCACACAGATAATTCAAGGAAAACGTTCTGGTCTTACGGGTGATGTAGGTTTT		95
Sbjct 28347			
Query 960	TGTCTGACAATAGTGAAGCGGTGACAGCATATCAGACGGCTCAGTCCTGCTATATTACTG		10

Sbjct	28287	TGTCTGACAATACTGAAGCGGTGACAGCATATCAGACGGCTCAGTCCTGCTATATTACTG	28
Query	1020	TCATGGCCACTATGGCAGATGACCAGATCAGGTTAAATTCCCCGATAATCCGTCGAAGT	10
Sbjct	28227	TCATGGCCACTATGGCAGATGACCAGATCAGGTTAAATTCCCCGATAATCCGTCGAAGT	28
Query	1080	CTGAGGGATGGAAGGAAGGTGAAGGCTGTTCTGAAAGGAATAAAAGTGACATCATGCCCT	11
Sbjct	28167	CTGAGGGATGGAAGGAAGGTGAAGGCTGTTCTGAAAGGAATAAAAGTGACATCATGCCCT	28
Query	1140	CTTTTCTGGCTCCGGAGCAATTACTTTACTTTCTGCAG	1181
Sbjct	28107	CTTTTCTGGCTCCGGAGCAATTACTTTACTTTCTGCAG	28066

>gb|AF074613.1| D Escherichia coli O157:H7 plasmid pO157, complete sequence
Length=92077

Score = 2111 bits (2340), Expect = 0.0
Identities = 1178/1182 (99%), Gaps = 1/1182 (0%)
Strand=Plus/Minus

Query	1	CTGCAGGAGA-TGG TTGCCCATCCCAGCGCGCTCCAGCT	59
Sbjct	19435	CTGCAGGAGAGTGGAAAAAAAGCCAAAATAAAAAATGCCCATCCCAGCGCGCTCCAGCT	19
Query	60	GAAAGTAGGCCTGTTCTGTCGGTATTTAAATGCATTGACCGTCCCCGTATTTAAACAAAT	11
Sbjct	19375	GAAAGTAGGCCTGTTCTGTCGGTATTTAAATGCATTGACCGTCCCCGTATTTAAACAAAT	19
Query	120	GTGATAAAATTACTCCGTTACCGGAAACCGCTGAACAAAATTGGGCTGAAAGAGGATC	17
Sbjct	19315	GTGATAAAATTACTCCGTTACCGGAAACCGCTGAACAAAATTGGGCTGAAAGAGGATC	19
Query	180	CGCCGTTATCTGTTGCATTCCTCTAGCCTGACTAGCCAGAGACACAATGATCTGTGCC	23
Sbjct	19255	CGCCGTTATCTGTTGCATTCCTCTAGCCTGACTAGCCAGAGACACAATGATCTGTGCC	19
Query	240	GTTCTGTTAATATCAAACCGGTACTCAATATCTCTGCGCTGGCTGCCATCATCCGG	29
Sbjct	19195	GTTCTGTTAATATCAAACCGGTACTCAATATCTCTGCGCTGGCTGCCATCATCCGG	19
Query	300	AAGCGTCCGGTCGGGATAAAAAATCGCGAGTGCGCCGGTCCATGCAGACACATCCCCC	35
Sbjct	19135	AAGCGTCCGGTCGGGATAAAAAATCGCGAGTGCGCCGGTCCATGCAGACACATCCCCC	19
Query	360	ACGGGTAACAGCGTCCCTGTACATTCTCTGAATGACATCAGGGATCCGCCGTCTCA	41
Sbjct	19075	ACGGGTAACAGCGTCCCTGTACATTCTCTGAATGACATCAGGGATCCGCCGTCTCA	19
Query	420	CTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAACGCTTCA	47
Sbjct	19015	CTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAACGCTTCA	18
Query	480	TTTCCGAAGGCATGACCACACACTGGCAATCCGGTAGACCGGTAACGCTGGAAAAGG	53
Sbjct	18955	TTTCCGAAGGCATGACCACACACTGGCAATCCGGTAGACCGGTAACGCTGGAAAAGG	18
Query	540	GCACCTGCCATTAACACATCTCGCTCATCCCAGGTGTTCTGCTGCTGACGCAGACGT	59
Sbjct	18895	GCACCTGCCATTAACACATCTCGCTCATCCCAGGTGTTCTGCTGCTGACGCAGACGT	18
Query	600	GCTTCGTATTCTCACGCCGGCGCCACCACGAGCCAGCAGCAGAACATGATTCCTCCATC	65
Sbjct	18835	GCTTCGTATTCTCACGCCGGCGCCACCACGAGCCAGCAGCAGAACATGATTCCTCCATC	18
Query	660	TTCAGCTGATAACAATACAGCAGCATAAATTCTGTCCTTTGGGACGTAGCATCCCC	71
Sbjct	18775	TTCAGCTGATAACAATACAGCAGCATAAATTCTGTCCTTTGGGACGTAGCATCCCC	18
Query	720	ACCTGAACGATAAGCGGAACATTGCTGATGCAGCCCAGGCCTGGATATGCAGGGGT	77
Sbjct	18715	ACCTGAACGATAAGCGGAACATTGCTGATGCAGCCCAGGCCTGGATATGCAGGGGT	18
Query	780	AACGGTCGATGGCTTCATTATGCAATGCCGGCAGTCGAAACCCGGTGGATAACCGTT	83
Sbjct	18655	AACGGTCGATGGCTTCATTATGCAATGCCGGCAGTCGAAACCCGGTGGATAACCGTT	18
Query	840	ACCGGTGTCCTGACACCTCCGCCATCAGATGCGCCATCATGGGTGAGATAGGCACAACA	89

Sbjct	18595	ACCGGTGTCCTGACACCTTCCGCCATCAGATGCGCCATCATGGCTGAGCTAGGCACAACA	18
Query	900	ATGAAATCACACAGATAATTCAAGGGAAAACGTTCTGGCTTACGGGTGATGTAGGTTTT	95
Sbjct	18535	ATGAAATCACACAGATAATTCAAGGGAAAACGTTCTGGCTTACGGGTGATGTAGGTTTT	18
Query	960	TGTCTGACAATAGTGAAGCGGTGACAGCATATCAGACGGCTCAGTCCTGCTATATTACTG	10
Sbjct	18475	TGTCTGACAATACTGAAGCGGTGACAGCATATCAGACGGCTCAGTCCTGCTATATTACTG	18
Query	1020	TCATGGCCACTATGGCAGATGACCAGATCAGGTTAAATTCCCCGATAATCCGTCGAAGT	10
Sbjct	18415	TCATGGCCACTATGGCAGATGACCAGATCAGGTTAAATTCCCCGATAATCCGTCGAAGT	18
Query	1080	CTGAGGATGGAAGGAAGGTGAAGGCTGTTCCCTGAAAGGAATAAAAGTGACATCATGCCCT	11
Sbjct	18355	CTGAGGATGGAAGGAAGGTGAAGGCTGTTCCCTGAAAGGAATAAAAGTGACATCATGCCCT	18
Query	1140	CTTTTTCTGGCTTCCGGACCAATTACTTTCTCTGCAG	1181
Sbjct	18295	CTTTTTCTGGCTTCCGGACCAATTACTTTCTCTGCAG	18254

>emb|Y11275.1|EC74PO157 G E.coli 7.4 kb DNA from plasmid pO157
Length=7395

Score = 2111 bits (2340), Expect = 0.0
Identities = 1178/1182 (99%), Gaps = 1/1182 (0%)
Strand=Plus/Minus

Sbjct	2166	ACCTGAACGATAAGCGGAACATGTCTGCTGATGCAGGCCAGGCGTGGATATGCAGGGGT	210
Query	780	AACGGTCGCATGGCTTCATTATGCAATGCGGGCCAGTCGAAACCCGGTGGATAACCGTT	839
Sbjct	2106	AACGGTCGCATGGCTTCATTATGCAATGCGGGCCAGTCGAAACCCGGTGGATAACCGTT	204
Query	840	ACCGGTGTCCTGACACCTTCCGCCATCAGATGCGCCATCATGGGTGAGATAGGCACAACA	899
Sbjct	2046	ACCGGTGTCCTGACACCTTCCGCCATCAGATGCGCCATCATGGCTGAGCTAGGCACAACA	198
Query	900	ATGAAATCACACAGATAATTCAAGGGAAAACGTTCTGGCTTACGGGTGATGTAGGTTTT	959
Sbjct	1986	ATGAAATCACACAGATAATTCAAGGGAAAACGTTCTGGCTTACGGGTGATGTAGGTTTT	192
Query	960	TGTCTGACAATAGTGAAGCGGTGACAGCATATCAGACGGCTCAGTCCTGCTATATTACTG	101
Sbjct	1926	TGTCTGACAATAGTGAAGCGGTGACAGCATATCAGACGGCTCAGTCCTGCTATATTACTG	186
Query	1020	TCATGGCCACTATGGCAGATGACCAGATCAGGTTAAATTCCCGATAATCCGTCGAAGT	107
Sbjct	1866	TCATGGCCACTATGGCAGATGACCAGATCAGGTTAAATTCCCGATAATCCGTCGAAGT	180
Query	1080	CTGAGGATGGAAGGAAGGTGAAGGCTGTTCTGAAAGGAATAAAAGTGACATCATGCCCT	113
Sbjct	1806	CTGAGGATGGAAGGAAGGTGAAGGCTGTTCTGAAAGGAATAAAAGTGACATCATGCCCT	174
Query	1140	CTTTTCTGGCTTCCGGAGCAATTACTTTACTTTCTCTGCAG	1181
Sbjct	1746	CTTTTCTGGCTTCCGGAGCAATTACTTTACTTTCTCTGCAG	1705

>dbj|AB011549.2| D Escherichia coli O157:H7 str. Sakai plasmid pO157 DNA, complete sequence
Length=92721

Score = 2111 bits (2340), Expect = 0.0
Identities = 1178/1182 (99%), Gaps = 1/1182 (0%)
Strand=Plus/Minus

Query	1	CTGCAGGAGA-TGG CTGCAGGAGA-TGG TTGCCCATCCAGCGCGCTCCAGCT	59
Sbjct	88950	CTGCAGGAGAGTGGAAAAAAAGCCAAAATAAAATGCCCATCCAGCGCGCTCCAGCT	88
Query	60	GAAAGTAGGCCTGTTCTGTCGGTATTAAATGCATTGACCGTCCCCGTATTAAACAAT	11
Sbjct	88890	GAAAGTAGGCCTGTTCTGTCGGTATTAAATGCATTGACCGTCCCCGTATTAAACAAT	88
Query	120	GTGATAAAATTACTCCGTTACCGGAAACCGCTGAACAAAATTCCGGCTGAAAAGAGGATC	17
Sbjct	88830	GTGATAAAATTACTCCGTTACCGGAAACCGCTGAACAAAATTCCGGCTGAAAAGAGGATC	88
Query	180	CGCCGTATCTGTTGCATTCCCTTAGCCTGACTAGCCAGAGACACAATGATCTGTGCC	23
Sbjct	88770	CGCCGTATCTGTTGCATTCCCTTAGCCTGACTAGCCAGAGACACAATGATCTGTGCC	88
Query	240	GTTCTGTTAATATCAAACCGGTACTCAATATCTCTGGCGCTGGCTGCCATCATCCGG	29
Sbjct	88710	GTTCTGTTAATATCAAACCGGTACTCAATATCTCTGGCGCTGGCTGCCATCATCCGG	88
Query	300	AAGCGTCCGGTCGGGATAAAAAATCGCCAGTGCGCCGGTCCATGCAGACACATCCCCC	35
Sbjct	88650	AAGCGTCCGGTCGGGATAAAAAATCGCCAGTGCGCCGGTCCATGCAGACACATCCCCC	88
Query	360	ACGGGTAACAGCGTCCCTGTCACATTCTCTGAATGACATCAGGGATCCGCCGTCTCA	41
Sbjct	88590	ACGGGTAACAGCGTCCCTGTCACATTCTCTGAATGACATCAGGGATCCGCCGTCTCA	88
Query	420	CTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAACGCTTC	47
Sbjct	88530	CTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAACGCTTC	88
Query	480	TTTCCGAAGGCATGACCACACACTGGCAATCCGTTAGACCGGTAACGCTGGAAAAGG	53
Sbjct	88470	TTTCCGAAGGCATGACCACACACTGGCAATCCGTTAGACCGGTAACGCTGGAAAAGG	88
Query	540	GCACCTGCCATTAACACATCTCCGCTCATCAGGTTCTGCTGACGCAGACGT	59
Sbjct	88410	GCACCTGCCATTAACACATCTCCGCTCATCAGGTTCTGCTGACGCAGACGT	88

Query	600	GCTTCGTATTCTTCAGCCGGCGCCACCACGAGCCAGCAAATGATTCCCTCCATC	65
Sbjct	88350	GCTTCGTATTCTTCAGCCGGCGCCACCACGAGCCAGCAAATGATTCCCTCCATC	88
Query	660	TTCAGCTGATAACAATACACGCAGCAATAATTCTATGTCCTTTCCGGGACCTAGCATCCCC	71
Sbjct	88290	TTCAGCTGATAACAATACACGCAGCATAAAATTCTATGTCCTTTCCGGGACGTAGCATCCCC	88
Query	720	ACCTGAACGATAAGCGGAACATTGTCGCTGATGCAGCCCAGGCGTGGATATGCAGGGGT	77
Sbjct	88230	ACCTGAACGATAAGCGGAACATTGTCGCTGATGCAGCCCAGGCGTGGATATGCAGGGGT	88
Query	780	AACGGTCCGATGGCTCATTATGCAATGCAGGGCCAGTCGAAACCCGGTGGATAACCGTT	83
Sbjct	88170	AACGGTCCGATGGCTCATTATGCAATGCAGGGCCAGTCGAAACCCGGTGGATAACCGTT	88
Query	840	ACCGGGTGCCTGACACCTTCCGCCATCAGATGCGCCATCATGGTGAGATAGGCACAACA	89
Sbjct	88110	ACCGGGTGCCTGACACCTTCCGCCATCAGATGCGCCATCATGGTGAGCTAGGCACAACA	88
Query	900	ATGAAATCACACAGATAATTCAAGGAAAACGTTCTGGCTTACGGGTGATGTAGGTTTT	95
Sbjct	88050	ATGAAATCACACAGATAATTCAAGGAAAACGTTCTGGCTTACGGGTGATGTAGGTTTT	87
Query	960	TGTCTGACAATAGTGAAGCGGTGACAGCATATCAGACGGCTCAGTCCTGCTATATTACTG	10
Sbjct	87990	TGTCTGACAATAGTGAAGCGGTGACAGCATATCAGACGGCTCAGTCCTGCTATATTACTG	87
Query	1020	TCATGGCCACTATGGCAGATGACCAGATCAGGTTAAATTCCCCGATAATCCGTCGAAGT	10
Sbjct	87930	TCATGGCCACTATGGCAGATGACCAGATCAGGTTAAATTCCCCGATAATCCGTCGAAGT	87
Query	1080	CTGAGGATGGAAGGAAGGTGAAGGCTTCTGAAAGGAATAAAAGTGACATCATGCCCT	11
Sbjct	87870	CTGAGGATGGAAGGAAGGTGAAGGCTTCTGAAAGGAATAAAAGTGACATCATGCCCT	87
Query	1140	CTTTTCTGGCTTCCGGAGCAATTACTTTCTGCAG	1181
Sbjct	87810	CTTTTCTGGCTTCCGGAGCAATTACTTTCTGCAG	87769

>gb|AF043470.1|AF043470 G Escherichia coli plasmid pO157 ecf4 gene, partial c-ecf2, and ecf1 genes, complete cds
Length=5612

GENE ID: 5290933 SF0157_p16 | w0016 [Escherichia coli]
(10 or fewer PubMed links)

Score = 2102 bits (2330), Expect = 0.0
Identities = 1176/1182 (99%), Gaps = 1/1182 (0%)
Strand=Plus/Plus

Query	1	CTGCAGGAGA-TGG	TTGCCCATCCCAGCGCGCTCCAGCT	59
Sbjct	2404	CTGCAGGAGAGTGGAAAAAAAGC AAAAATTGGCCATCCCAGCGCGCTCCAGCT		246
Query	60	GAAAAGTAGGCCTGTTCTGTCCGGTATTTAAATGCATTGACCGTCCCCGTATTTAAACAAAT		119
Sbjct	2464	GAAAAGTAGGCCTGTTCTGTCCGGTATTTAAATGCATTGACCGTCCCCGTATTTAAACAAAT		252
Query	120	GTGATAAAATTACTCCGT TACCGGAAAACCGCTGAACAAAATTGGGCTGAAAAGAGGATC		179
Sbjct	2524	GTGATAAAATTACTCCGT TACCGGAAAACCGCTGAACAAAATTGGGCTGAAAAGAGGATC		258
Query	180	CGCCGTTATCTGTTGCATTCCCCCTAGCCTGACTAGCAGAGACACAATGATCTGTGCC		239
Sbjct	2584	CGCCGTTATCTGTTGCATTCCCCCTAGCCTGACTAGCAGAGACACAATGATCTGTGCC		264
Query	240	GTTCTGTTAATATCAAACCGTACTCAATATCTCTGGCGCTGGCTGCCATCATCCGG		299
Sbjct	2644	GTTCTGTTAATATCAAACCGTACTCAATATCTCTGGCGCTGGCTGCCATCATCCGG		270
Query	300	AAGCGTTCCGGTCGGGATAAAAATCGCGAGTGC GCGCCGGTCCATGCAGACACATCCCCC		359
Sbjct	2704	AAGCGTTCCGGTCGGGATAAAAATCGCGAGTGC GCGCCGGTCCATGCAGACACATCCCCC		276
Query	360	ACGGGTAAACAGCGTCCCTGTCA CATTCTGAATGACATCAGGGATCCCGCCGTCTCA		419
Sbjct	2764	ACGGGTAAACAGCGTCCCTGTCA CATTCTGAATGACATCAGGGATCCCGCCGTCTCA		282

Query	420	CTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAAACGTTCA	479
Sbjct	2824	CTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAAACGTTCA	288
Query	480	TTTCCGAAGGCATGACCACCACTGGCAATCCGGTAGACCGGTAAACGCTGGGAAAAGG	539
Sbjct	2884	TTTCCGAAGGCATGACCACCACTGGCAATCCGGTAGACCGGTAAACGCTGGGAAAAGG	294
Query	540	GCACCTGCCATTAACACATCTCCGCTCATCCCAGGTGTTGCTGCTGACGCAGACGT	599
Sbjct	2944	GCACCTGCCATTAACACATCTCCGCTCATCCCAGGTGTTGCTGCTGACGCAGACGT	300
Query	600	GCTTCGTATTCTCACGCCCGGCCACCACGAGCCAGCGAAATGATTCCTCCATC	659
Sbjct	3004	GCTTCGTATTCTCACGCCCGGCCACCACGAGCCAGCGAAATGATTCCTCCATC	306
Query	660	TTCAGCTGATACAATACACGCAGCATAAATTATGTCCTTTGGGACGTAGCATCCCC	719
Sbjct	3064	TTCAGCTGATACAATACACGCAGCATAAATTATGTCCTTTGGGACGTAGCATCCCC	312
Query	720	ACCTGAACGATAAGCGGAACATTGCTGCTGATGCAGCCCAGGCGTGGATATGCAGGGGT	779
Sbjct	3124	ACCTGAACGATAAGCGGAACATTGCTGCTGATGCAGCCCAGGCGTGGATATGCAGGGGT	318
Query	780	AACGGTCGCATGGCTTCATTATGCAATGCCGGCCAGTCGAAACCCGGTGGATAACCGTT	839
Sbjct	3184	AACGGTCGCATGGCTTCATTATGCAATGCCGGCCAGTCGAAACCCGGTGGATAACCGTT	324
Query	840	ACCGGTGCTGACACCTCCGCCATCAGATGCCCATCATGGGTGAGATAGGCACAACA	899
Sbjct	3244	ACCGGTGCTGACACCTCCGCCATCAGATGCCCATCATGGGTGAGCTAGGCACAACA	330
Query	900	ATGAAATCACACAGATAATTCAAGGAAACGTTCTGGCTTACGGTGATGTAGGTTTT	959
Sbjct	3304	ATGAAATCACACAGATAATTCAAGGAAACGTTCTGGCTTACGGTGATGTAGGTTTT	336
Query	960	TGTCTGACAATAGTGAAGCGGTGACAGCATATCAGACGGCTCAGTCCTGCTATATTACTG	101
Sbjct	3364	TGTCTGACAATAGTGAAGCGGTGACAGCATATCAGACGGCTCAGTCCTGCTATATTACTG	342
Query	1020	TCATGGCCACTATGGCAGATGACCAGATCAGGTTAAATTCCCGATAATCCGTCGAAAGT	107
Sbjct	3424	TCATGGCCACTATGGCAGATGACCAGATCAGGTTAAATTCCCGATAATCCGTCGAAAGT	348
Query	1080	CTGAGGATGGAAGGAAGGTGAAGGCTGTTCTGAAAGGAATAAAAGTGACATCATGCCCT	113
Sbjct	3484	CTGAGGATGGAAGGAAGGTGAAGGCTGTTCTGAAAGGAATAAAAGTGACATCATGCCCT	354
Query	1140	CTTTTCTGGCTCCGGAGCAATTAACTTTCTGAG	1181
Sbjct	3544	CTTTTCTGGCTCCGGAGCAATTAACTTTCTGAG	3585

>gb|CP000035.11 | Shigella dysenteriae Sd197 plasmid pSD1_197, complete sequence
Length=182726

Score = 138 bits (152), Expect = 6e-29
Identities = 207/289 (71%), Gaps = 4/289 (1%)
Strand=Plus/Minus

Query	237	GCCGTTCTGTTAATATCAAACCGTACTCAATATCTCTGGCGCTGGCT-GCCATCAT	29
Sbjct	87991	GCAGTTTATTAAATATCAAACCGCTCTCTATATCCTGTTTGCG-CTGGCGAGCCATCTG	87
Query	296	CCGGAAGCGTCCGG-TCGGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACAT	35
Sbjct	87932	ATAAAAAACGTCCAGGGTCATTA-AAAAAAATCATTCAAGGGCGCACATCCATGCGTGCTTAT	87
Query	355	CCCCCACGGGTAACAGCGTCCCTGTACACATTCTGTAATGACATCAGGGATCCGCCCG	41
Sbjct	87873	TACCTGCTGGTAACAATGTCCGGCTGGTTGTTGATAAACATCAGGGATTCCACCAA	87
Query	415	TCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAACG	47
Sbjct	87813	TCTGACTGGCCAGTACAGGCACAGAAAATGCCGATGCTCTGCGCAGTACCATACCAAACG	87
Query	475	CTTCATTTCCGAAGGCATGACCACCACTGGCAATCCGGTAGACCGG	523
Sbjct	87753	ATTGTTCTGAAGGCAGAACCAACAGACTGGCAACCGATAACGGG	87705

>gb|CP001064.1| Escherichia coli 53638 plasmid p53638_226, complete sequence
Length=225683

Features in this part of subject sequence:
UDP-sugar hydrolase

Score = 132 bits (146), Expect = 3e-27
Identities = 206/289 (71%), Gaps = 4/289 (1%)
Strand=Plus/Plus

Query 237	GCCGTTCTGTTAATATCAAACCGTACTCAATATCTTCTCTGGCGCTGGCT-GCCATCAT	2
Sbjct 115503	GCAGTTTATTAAATATCAAACCGCTCTCTATATCCTGTTTGC-CTGGCGAGCCATCTG	1
Query 296	CCGGAAGCGTTCGG-TCGGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACAT	3
Sbjct 115562	ATAAAAAACGCCAGGGTCATTA-AAAAAAATCATTAGGGCGCACATCCATGCGTGCTTAT	1
Query 355	CCCCCACGGGTAAACAGCGTCCCTGTACATTCTCTGAATGACATCAGGGATCCC GCCCG	4
Sbjct 115621	TACCTGCTGGTAACAATGTCCGGTCTGGTTGTTCTGAATAACATCAGGGATTCCACCAA	1
Query 415	TCTCACTGGCGATAACGGGACGCCGGAGACTGACGCTTCAGCCAGTACCCATACCAAACG	4
Sbjct 115681	TCTGACTGGCCAGTACAGGCACAGAAAATGCCGATGCTTCTGCCAGTACCCATACCAAACG	1
Query 475	CTTCATTTCCGAAGGCATGACCACCAACTGGCAATCCGGTAGACCGG	523
Sbjct 115741	ATT CGTTTCTGAAGGCAGAACCAACCAGACTGGCAACCCGATATACGGG	115789

>gb|CP001062.1| Shigella boydii CDC 3083-94 plasmid pBS512_211, complete sequence
Length=210919

Features in this part of subject sequence:
putative glycosyl transferase, group 1 family protein

Score = 132 bits (146), Expect = 3e-27
Identities = 206/289 (71%), Gaps = 4/289 (1%)
Strand=Plus/Minus

Query 237	GCCGTTCTGTTAATATCAAACCGTACTCAATATCTTCTCTGGCGCTGGCT-GCCATCAT	2
Sbjct 176254	GCAGTTTATTAAATATCAAACCGCTCTCTATATCCTGTTTGC-CTGGCGAGCCATCTG	1
Query 296	CCGGAAGCGTTCGG-TCGGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACAT	3
Sbjct 176195	ATAAAAAACGCCAGGGTCATTA-AAAAAAATCATTAGGGCGCACATCCATGCGTGCTTAT	1
Query 355	CCCCCACGGGTAAACAGCGTCCCTGTACATTCTCTGAATGACATCAGGGATCCC GCCCG	4
Sbjct 176136	TACCTGCTGGTAACAATGTCCGGTCTGGTTGTTCTGAATAACATCAGGGATTCCACCAA	1
Query 415	TCTCACTGGCGATAACGGGACGCCGGAGACTGACGCTTCAGCCAGTACCCATACCAAACG	4
Sbjct 176076	TCTGACTGGCCAGTACAGGCACAGAAAATGCCGATGCTTCTGCCAGTACCCATACCAAACG	1
Query 475	CTTCATTTCCGAAGGCATGACCACCAACTGGCAATCCGGTAGACCGG	523
Sbjct 176016	ATT CGTTTCTGAAGGCAGAACCAACCAGACTGGCAACCCGATATACGGG	175968

>gb|AF386526.1| Shigella flexneri 2a str. 301 virulence plasmid pCP301, complete sequence
Length=221618

Features in this part of subject sequence:
UDP-sugar hydrolase

Score = 132 bits (146), Expect = 3e-27
Identities = 206/289 (71%), Gaps = 4/289 (1%)
Strand=Plus/Minus

Query 237	GCCGTTCTGTTAATATCAAACCGTACTCAATATCTTCTCTGGCGCTGGCT-GCCATCAT	2
Sbjct 193608	GCAGTTTATTAAATATCAAACCGCTCTCTATATCCTGTTTGC-CTGGCGAGCCATCTG	1
Query 296	CCGGAAGCGTTCGG-TCGGGATAAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACAT	3

Sbjct	193549		ATAAAAACGCCAGGGTCATTA-AAAAATCATTCAAGGGCGCACATCCATGCGTGCTTAT	1
Query	355		CCCCCACGGGTAAACAGCGTCCCTGTCACATTCTCTGAATGACATCAGGGATCCGCCCG	4
Sbjct	193490		TACCTGCTGGTAACAATGTCCCGGTCTGGTTATTCTGAATAACATCAGGGATTCCACCAA	1
Query	415		TCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAACG	4
Sbjct	193430		TCTGACTGGCCAGTACAGGCACAGAAAATGCCGATGCTTCTGCCAGTACCATACCAAACG	1
Query	475		CTTCATTTCCGAAGGCATGACCACCAACTGGCAATCCGGTAGACCGG	523
Sbjct	193370		ATTCGTTTCTGAAGGCAGAACCAACCAGACTGGCAACCCGATATACGGG	193322

>gb|AY206446.1| Shigella flexneri plasmid pINV_F6_M1382 ORF186 (ORF186), VirK (virK), and MsbB2 (msbB2) genes, complete cds
Length=3815

Score = 132 bits (146), Expect = 3e-27
Identities = 206/289 (71%), Gaps = 4/289 (1%)
Strand=Plus/Minus

Query	237		GCCGTTCTGTTAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCT-GCCATCAT	295
Sbjct	1817		GCAGTTTATTAAATATCAAACCGCTCTTCTATATCCTGTTTGC-CTGGCGAGCCATCTG	175
Query	296		CCGGAAGCGTTCCGG-TCGGGATAAAAAATCGCGCAGTGCAGCCGGTCCATGCAGACACAT	354
Sbjct	1758		ATAAAAACGCCAGGGTCATTA-AAAAATCATTCAAGGGCGCACATCCATGCGTGCTTAT	170
Query	355		CCCCCACGGGTAAACAGCGTCCCTGTCACATTCTCTGAATGACATCAGGGATCCGCCCG	414
Sbjct	1699		TACCTGCTGGTAACAATGTCCCGGTCTGGTTCTGAATAACATCAGGGATTCCACCAA	164
Query	415		TCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAACG	474
Sbjct	1639		TCTGACTGGCCAGTACAGGCACAGAAAATGCCGATGCTTCTGCCAGTACCATACCAAACG	158
Query	475		CTTCATTTCCGAAGGCATGACCACCAACTGGCAATCCGGTAGACCGG	523
Sbjct	1579		ATTCGTTTCTGAAGGCAGAACCAACCAGACTGGCAACCCGATATACGGG	1531

>emb|AL391753.1|SFPWR100 D Shigella flexneri virulence plasmid pWR100: from 1 Length=213494

Features in this part of subject sequence:
unnamed protein product

Score = 132 bits (146), Expect = 3e-27
Identities = 206/289 (71%), Gaps = 4/289 (1%)
Strand=Plus/Minus

Query	237		GCCGTTCTGTTAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCT-GCCATCAT	2
Sbjct	187268		GCAGTTTATTAAATATCAAACCGCTCTTCTATATCCTGTTTGC-CTGGCGAGCCATCTG	1
Query	296		CCGGAAGCGTTCCGG-TCGGGATAAAAAATCGCGCAGTGCAGCCGGTCCATGCAGACACAT	3
Sbjct	187209		ATAAAAACGCCAGGGTCATTA-AAAAATCATTCAAGGGCGCACATCCATGCGTGCTTAT	1
Query	355		CCCCCACGGGTAAACAGCGTCCCTGTCACATTCTCTGAATGACATCAGGGATCCGCCCG	4
Sbjct	187150		TACCTGCTGGTAACAATGTCCCGGTCTGGTTATTCTGAATAACATCAGGGATTCCACCAA	1
Query	415		TCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAACG	4
Sbjct	187090		TCTGACTGGCCAGTACAGGCACAGAAAATGCCGATGCTTCTGCCAGTACCATACCAAACG	1
Query	475		CTTCATTTCCGAAGGCATGACCACCAACTGGCAATCCGGTAGACCGG	523
Sbjct	187030		ATTCGTTTCTGAAGGCAGAACCAACCAGACTGGCAACCCGATATACGGG	186982

>gb|AF348706.1| D Shigella flexneri 5a plasmid virulence plasmid pWR501, comp sequence
Length=221851

Features in this part of subject sequence:
UDP-sugar hydrolase

Score = 132 bits (146), Expect = 3e-27
Identities = 206/289 (71%), Gaps = 4/289 (1%)
Strand=Plus/Minus

>gb|AY879342.1| D Shigella flexneri plasmid pSF5, complete sequence
Length=136694

Score = 132 bits (146), Expect = 3e-27
Identities = 206/289 (71%), Gaps = 4/289 (1%)
Strand=Plus/Plus

>gb|CP000037.1| D Shigella boydii Sb227 plasmid pSB4_227, complete sequence
Length=126697

Score = 132 bits (146), Expect = 3e-27
Identities = 206/289 (71%), Gaps = 4/289 (1%)
Strand=Plus/Minus

Sbjct 97908 ATTCGTTTCTGAAGGCAGAACCAACAGACTGGCAACCCGATATACGGG 97860

>gb|CP000039.1| D Shigella sonnei Ss046 plasmid pSS_046, complete sequence
Length=214396

Features in this part of subject sequence:
conserved hypothetical protein

Score = 132 bits (146), Expect = 3e-27
Identities = 206/289 (71%), Gaps = 4/289 (1%)
Strand=Plus/Minus

Query 237	GCCGTTCTGTTAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCT-GCCATCAT	2
Sbjct 158570	GCAGTTTATTAAATATCAAACCGCTCTCTATATCCTGTTTGC-CTGGCGAGCCATCTG	1
Query 296	CCGGAAGCGTTCCGG-TCGGGATAAAAAATCGCGCAGTGCAGCGGTCCATGCAGACACAT	3
Sbjct 158511	ATAAAAAACGCCAGGGTCATTA-AAAAAAATCATTCAAGGGCGCACATCCATGCGTGCTTAT	1
Query 355	CCCCCACGGGTAAACAGCGTCCCTGTCACATTCTTGAATGACATCAGGGATCCCGCCCG	4
Sbjct 158452	TACCTGCTGGTAACAATGTCCGGTCTGGTTCTGAATAACATCAGGGATTCCACCAA	1
Query 415	TCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAACG	4
Sbjct 158392	TCTGACTGGCCAGTACAGGCACAGAAAATGCCATGCTTCTGCCAGTACCATACCAAACG	1
Query 475	CTTCATTTCCGAAGGCATGACCACCAACTGGCAATCCGGTAGACCGG	523
Sbjct 158332	ATTCGTTTCTGAAGGCAGAACCAACCAAGACTGGCAACCCGATATACGGG	158284

>dbj|D11025.1|SHFVIRK Shigella flexneri plasmid pMYSH6000 virK gene for virul-
complete cds
Length=1642

Score = 132 bits (146), Expect = 3e-27
Identities = 206/289 (71%), Gaps = 4/289 (1%)
Strand=Plus/Minus

Query 237	GCCGTTCTGTTAATATCAAACCGGTACTCAATATCTTCTCTGGCGCTGGCT-GCCATCAT	295
Sbjct 334	GCAGTTTATTAAATATCAAACCGCTCTCTATATCCTGTTTGC-CTGGCGAGCCATCTG	276
Query 296	CCGGAAGCGTTCCGG-TCGGGATAAAAAATCGCGCAGTGCAGCGGTCCATGCAGACACAT	354
Sbjct 275	ATAAAAAACGCCAGGGTCATTA-AAAAAAATCATTCAAGGGCGCACATCCATGCGTGCTTAT	217
Query 355	CCCCCACGGGTAAACAGCGTCCCTGTCACATTCTTGAATGACATCAGGGATCCCGCCCG	414
Sbjct 216	TACCTGCTGGTAACAATGTCCGGTCTGGTTATTCTGAATAACATCAGGGATTCCACCAA	157
Query 415	TCTCACTGGCGATAACGGGCACGCCGGAGACTGACGCTTCAGCCAGTACCATACCAAACG	474
Sbjct 156	TCTGACTGGCCAGTACAGGCACAGAAAATGCCATGCTTCTGCCAGTACCATACCAAACG	97
Query 475	CTTCATTTCCGAAGGCATGACCACCAACTGGCAATCCGGTAGACCGG	523
Sbjct 96	ATTCGTTTCTGAAGGCAGAACCAACCAAGACTGGCAACCCGATATACGGG	48

>gb|CP000799.1| D Escherichia coli E24377A plasmid pETEC_74, complete sequenc-
Length=74224

Score = 111 bits (122), Expect = 9e-21
Identities = 148/206 (71%), Gaps = 0/206 (0%)
Strand=Plus/Minus

Query 318	AAAAAAATCGCGCAGTGCAGCGGTCCATGCAGACACATCCCCACGGTAACAGCGTCCCT	37
Sbjct 61325	AAAAAAATCATTCAAGGGCGCACATCCATGCGTGCTTATTACCTGCTGGTAACAATGTCCCG	61
Query 378	GTCACATTCTTCTGAATGACATCAGGGATCCGCCGTCTACTGGCGATAACGGGCACG	43
Sbjct 61265	GTCTGGTTGTTCTGAATAACCTCAGGGATTCCACCAATCTGAGTGGCCACTACAGGCACA	61
Query 438	CCGGAGACTGACGCTTCAGCCAGTACCATACCAAACGCTTCATTTCCGAAGGCATGACC	49

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Sbjct 61205 GAAAATGCCGATGCTTCTGCCAGCACCATAACCAAAAGATTGTTCTGAAGGCAGAAC 61
Query 498 ACCACACTGGCAATCCGGTAGACCGG 523
Sbjct 61145 ACCAGACTGGCAACCCGATATACGGG 61120

```

>gb|CP000795.1| Escherichia coli E24377A plasmid pETEC_80, complete sequence
Length=79237

Score = 111 bits (122), Expect = 9e-21
Identities = 148/206 (71%), Gaps = 0/206 (0%)
Strand=Plus/Plus

```

Query 318 AAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACATCCCCCACGGTAACAGCGTCCT 37
Sbjct 37177 AAAAAATCATTCAAGGGCGCACATCCATGCGTGCTTATTACCTGCTGGTAACAATGTCCCG 37
Query 378 GTCACATTCTCTGAATGACATCAGGGATCCGCCGTCTCACTGGCGATAACGGGCACG 43
Sbjct 37237 GTCTGGTTGTTCTGAATAACCTCAGGGATTCCACCAATCTGAGTGGCCACTACAGGCACA 37
Query 438 CCGGAGACTGACGCTTCAGCCAGTACCATACCAAAACGCTTCATTTCCGAAGGCATGACC 49
Sbjct 37297 GAAAATGCCGATGCTTCTGCCAGCACCATAACCAAAAGATTGTTCTGAAGGCAGAAC 37
Query 498 ACCACACTGGCAATCCGGTAGACCGG 523
Sbjct 37357 ACCAGACTGGCAACCCGATATACGGG 37382

```

>dbj|AB255435.1| Escherichia coli plasmid pO86A1 DNA, complete sequence
Length=120730

Score = 111 bits (122), Expect = 9e-21
Identities = 148/206 (71%), Gaps = 0/206 (0%)
Strand=Plus/Plus

```

Query 318 AAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACATCCCCCACGGTAACAGCGTCCT 377
Sbjct 2154 AAAAAATCATTCAAGGGCGCACATCCATGCGTGCTTATTACCTGCTGGTAACAATGTCCCG 221
Query 378 GTCACATTCTCTGAATGACATCAGGGATCCGCCGTCTCACTGGCGATAACGGGCACG 437
Sbjct 2214 GTCTGGTTGTTCTGAATAACCTCAGGGATTCCACCAATCTGAGTGGCCACTACAGGCACA 227
Query 438 CCGGAGACTGACGCTTCAGCCAGTACCATACCAAAACGCTTCATTTCCGAAGGCATGACC 497
Sbjct 2274 GAAAATGCCGATGCTTCTGCCAGCACCATAACCAAAAGATTGTTCTGAAGGCAGAAC 233
Query 498 ACCACACTGGCAATCCGGTAGACCGG 523
Sbjct 2334 ACCAGACTGGCAACCCGATATACGGG 2359

```

>gb|AF134403.1|AF134403 Escherichia coli plasmid pAA2 Shf (shf), hexosyltrans (capU), and VirK (virK) genes, complete cds
Length=3500

Score = 111 bits (122), Expect = 9e-21
Identities = 148/206 (71%), Gaps = 0/206 (0%)
Strand=Plus/Minus

```

Query 318 AAAAAATCGCGCAGTGCGCCGGTCCATGCAGACACATCCCCCACGGTAACAGCGTCCT 377
Sbjct 2333 AAAAAATCATTCAAGGGCGCACATCCATGCGTGCTTATTACCTGCTGGTAACAATGTCCCG 227
Query 378 GTCACATTCTCTGAATGACATCAGGGATCCGCCGTCTCACTGGCGATAACGGGCACG 437
Sbjct 2273 GTCTGGTTGTTCTGAATAACCTCAGGGATTCCACCAATCTGAGTGGCCACTACAGGCACA 221
Query 438 CCGGAGACTGACGCTTCAGCCAGTACCATACCAAAACGCTTCATTTCCGAAGGCATGACC 497
Sbjct 2213 GAAAATGCCGATGCTTCTGCCAGCACCATAACCAAAAGATTGTTCTGAAGGCAGAAC 215
Query 498 ACCACACTGGCAATCCGGTAGACCGG 523
Sbjct 2153 ACCAGACTGGCAACCCGATATACGGG 2128

```

>emb|CR942285.1| D Escherichia coli plasmid pCoo
Length=98396

Score = 111 bits (122), Expect = 9e-21
Identities = 148/206 (71%), Gaps = 0/206 (0%)
Strand=Plus/Plus

Query 318	AAAAAAATCGCCAGTGCGCCGGTCCATGCAGACACATCCCCACGGGTAACAGCGTCCT	37
Sbjct 34153		34
Query 378	GTCACATTCTTCTGAATGACATCAGGGATCCC GCCGTCTCACTGGCGATAACGGGCACG	43
Sbjct 34213		34
Query 438	CCGGAGACTGACGTT CAGCCAGTACCATACCAAACGCTTCATTTCCGAAGGCATGACC	49
Sbjct 34273		34
Query 498	ACCACACTGGCAATCCGGTAGACCGG 523	
Sbjct 34333		

>gb|CP000800.1| D Escherichia coli E24377A, complete genome
Length=4979619

Features in this part of subject sequence:
putative glycosyl transferase, group 1 family protein

Score = 107 bits (118), Expect = 1e-19
Identities = 201/290 (69%), Gaps = 4/290 (1%)
Strand=Plus/Plus

Query 236	TGCCGTTCTGTTAATATCAAACCGGTACTCAATATCTTCTGGCGCTGGCT-GCCATCA	
Sbjct 4845818		
Query 295	TCCGGAAGCGTCCGG-TCGGGATAAAAATCGCCAGTGCGCCGGTCCATGCAGACACA	
Sbjct 4845877		
Query 354	TCCCCCACGGGTAACAGCGTCCCTGTCACATTCTCTGAATGACATCAGGGATCCGCC	
Sbjct 4845936		
Query 414	TTACTTGCTGGTAACAATGTCGGTCTGGTTCTGAATAACCTCAGGGCCACATCCATGCGTCTTA	
Sbjct 4845996		
Query 474	ATCTGAGTGGCCACTACAGGCACAGAAAATGCCGATGCTCTGCCAGCACCATACCAAAA	
Sbjct 4846056		
Query 474	GCTTCATTTCCGAAGGCATGACCACCAACTGGCAATCCGGTAGACCGG 523	
Sbjct 4846056		

>gb|AC133908.7| D Mus musculus chromosome 5, clone RP24-299L9, complete sequence
Length=214270

Score = 46.4 bits (50), Expect = 0.30
Identities = 28/30 (93%), Gaps = 0/30 (0%)
Strand=Plus/Minus

Query 4	CAGGAGATGGAAAAAAAGCCAAATAAAA 33	
Sbjct 185462		
	CAGGAGATGGAAAAAAAGCTGAAATAAAA 185433	

>gb|AC127327.4| D Mus musculus BAC clone RP23-254M18 from 5, complete sequence
Length=198433

Score = 46.4 bits (50), Expect = 0.30
Identities = 28/30 (93%), Gaps = 0/30 (0%)
Strand=Plus/Minus

Query 4	CAGGAGATGGAAAAAAAGCCAAATAAAA 33	
Sbjct 92692		
	CAGGAGATGGAAAAAAAGCTGAAATAAAA 92663	

>gb|EU025714.1| **D** *Salmo salar* retinoic acid receptor gamma a (Rarga), coiled-transcriptional coactivator a (Kiaal536), homeobox protein HoxC13aa (HoxC13aa), homeobox protein HoxC12aa (HoxC12aa), homeobox protein HoxC11aa (HoxC11aa), homeobox protein HoxC10aa (HoxC10aa), homeobox protein HoxC9aa (HoxC9aa), homeobox protein HoxC8aa (HoxC8aa), and homeobox protein HoxC6aa (HoxC6aa) genes, complete cds
Length=212839

Features in this part of subject sequence:
retinoic acid receptor gamma a

Score = 44.6 bits (48), Expect = 1.1
Identities = 27/29 (93%), Gaps = 0/29 (0%)
Strand=Plus/Plus

Query	1077	AGTCTGAGGATGGAAGGAAGGTGAAGGCT	1105
Sbjct	31660		31688

>emb|BX571861.1| **D** *Photorhabdus luminescens* subsp. *laumondii* TT01 complete genome segment 3/17
Length=342905

Features in this part of subject sequence:
unnamed protein product

Score = 44.6 bits (48), Expect = 1.1
Identities = 24/24 (100%), Gaps = 0/24 (0%)
Strand=Plus/Minus

Query	20	TTGCCCCATC	43
Sbjct	27988		27965

>gb|DQ192243.1| **G** *Operophtera brumata* reovirus segment 9, complete sequence
Length=1547

GENE ID: 5076725 OB RV_s9gp1 | hypothetical protein
[*Operophtera brumata* reovirus]

Score = 42.8 bits (46), Expect = 3.7
Identities = 26/28 (92%), Gaps = 0/28 (0%)
Strand=Plus/Minus

Query	247	TAATATCAAACCGGTACTCAATATCTTC	274
Sbjct	260		233

>gb|AC145866.3| **D** *Pan troglodytes* BAC clone RP43-21B7 from chromosome 7, complete sequence
Length=189814

Score = 42.8 bits (46), Expect = 3.7
Identities = 28/31 (90%), Gaps = 0/31 (0%)
Strand=Plus/Plus

Query	366	AACAGCGTCCCTGTCACATTCTCTGAATGA	396
Sbjct	137128		137158

>gb|AE015928.1| **D** *Bacteroides thetaiotaomicron* VPI-5482, complete genome
Length=6260361

Features in this part of subject sequence:
Histone-like bacterial DNA-binding protein

Score = 42.8 bits (46), Expect = 3.7
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

Query	855	CCTTCCGCCATCAGATGCGCCAT	877
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Sbjct 6023752 ||||||||||||||||||||| 6023774
CCTTCCGCCATCAGATGCGCCAT

>gb|AC004844.1| E D Homo sapiens PAC clone RP4-613I23 from 7p11-p13, complete
Length=141895

Score = 42.8 bits (46), Expect = 3.7
Identities = 28/31 (90%), Gaps = 0/31 (0%)
Strand=Plus/Plus

Query 366 AACAGCGTCCCTGT'CACATTCTTCTGAATGA 396
||||||| ||||||| ||||||| |||||||||||||
Sbjct 110633 AACAGAGTCCCTTCACATCCTTCTGAATGA 110663

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS,
GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

Posted date: Jul 20, 2008 5:48 PM

Number of letters in database: -1,464,584,741

Number of sequences in database: 7,064,549

Lambda K H
0.634 0.408 0.912

Gapped

Lambda K H
0.634 0.408 0.912

Matrix: blastn matrix:2 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 7064549

Number of Hits to DB: 12224137

Number of extensions: 604140

Number of successful extensions: 8350

Number of sequences better than 10: 0

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 8350

Number of HSP's successfully gapped: 0

Length of query: 1181

Length of database: 24305219031

Length adjustment: 36

Effective length of query: 1145

Effective length of database: 24050895267

Effective search space: 27538275080715

Effective search space used: 27538275080715

A: 0

X1: 22 (20.1 bits)

X2: 33 (29.8 bits)

X3: 110 (99.2 bits)

S1: 29 (27.4 bits)

S2: 45 (41.9 bits)